

Signatures of Dobzhansky-Muller Incompatibilities in the Genomes of Recombinant Inbred Lines

Maria Colomé-Tatché and Frank Johannes

Supplementary Figures and Tables

Supplementary Figures

A **B**

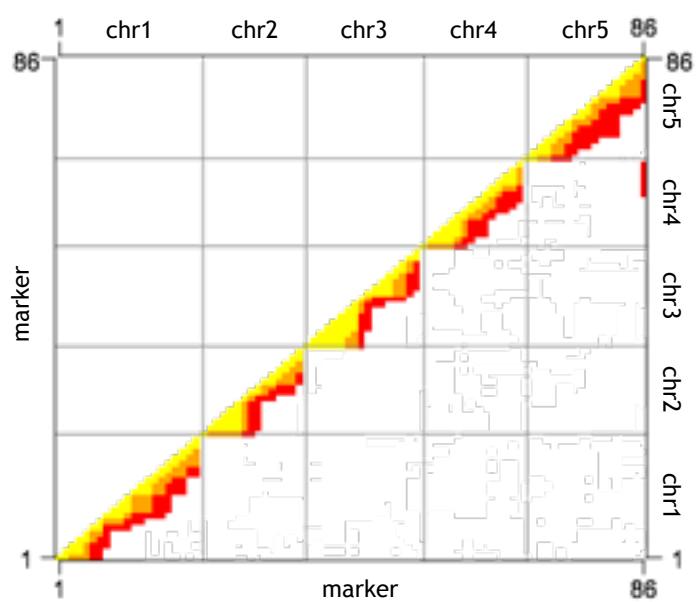
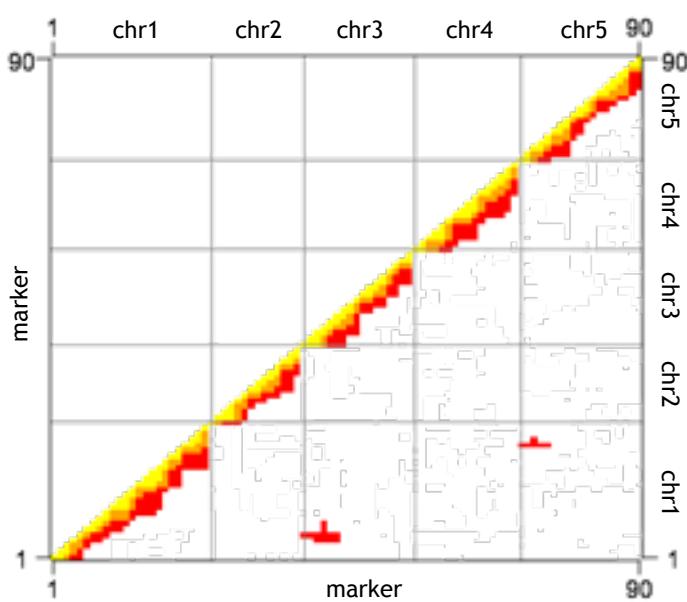


Figure S1. Transchromosomal (long-range) linkage disequilibrium for the Col × Cvi cross (A) and for the Col × Sha cross (B) Dark colors represent high LD between pairs of markers.

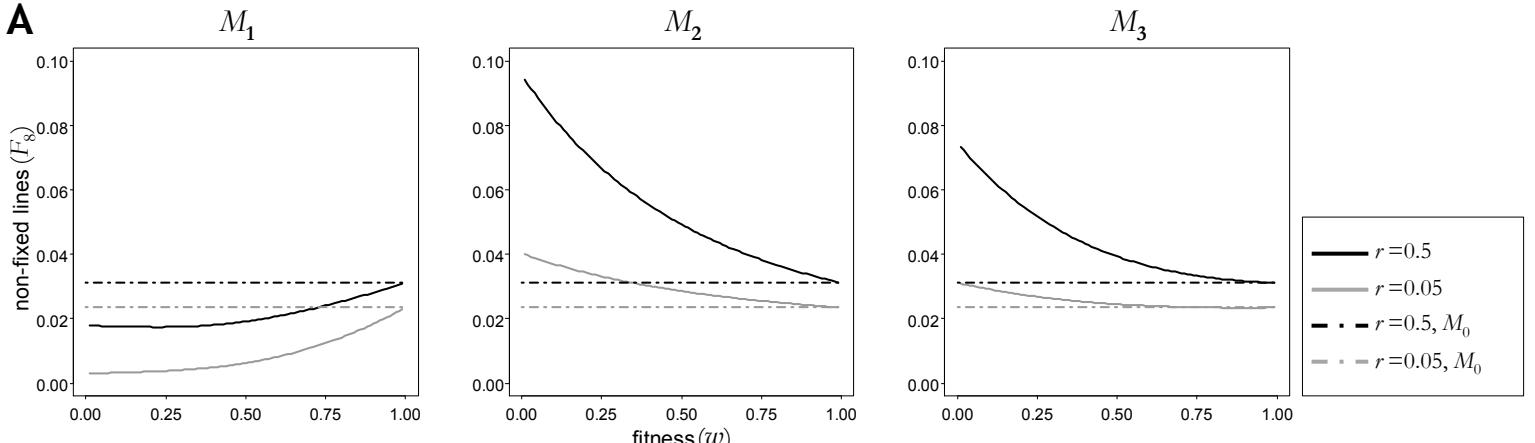
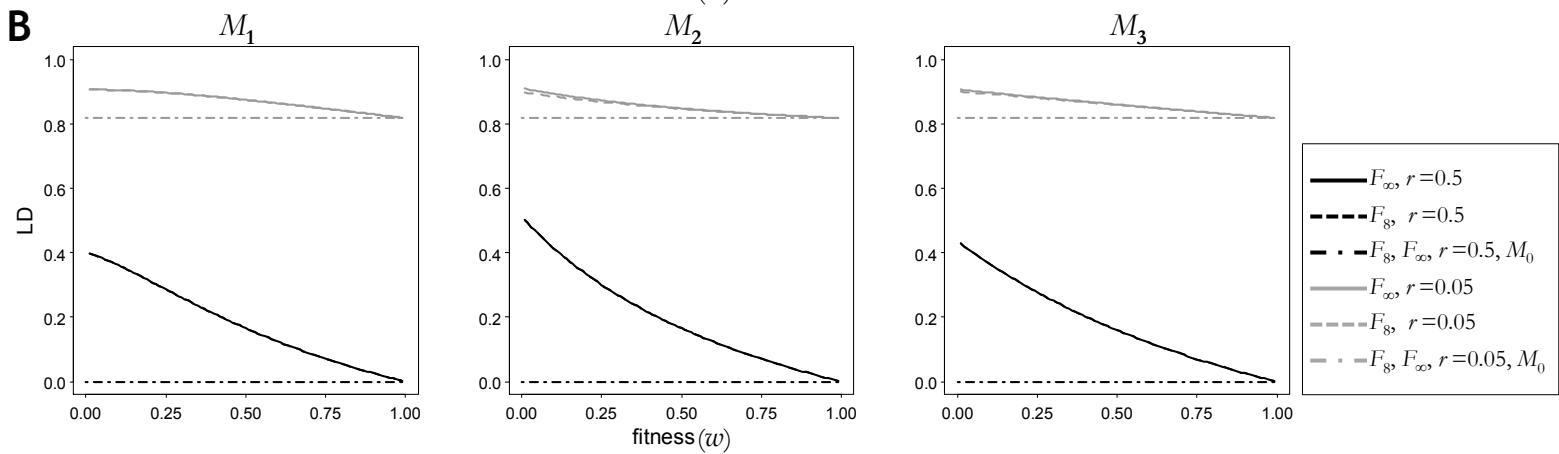
A**B**

Figure S2. Biased single seed descent (BSSD): (A) Proportion of diplotypes that have not yet reached fixation at generation F_8 versus fitness, for the incompatibility models with BSSD. **(B)** Linkage disequilibrium versus fitness for the incompatibility models with BSSD.

Supplementary Tables

Table S1. Results from the ML approach for the Cvi × Col cross. The tested models are ordered by decreasing AIC.

Cvi x Col

Model	Mode	w	w'	r	AIC	Incompatible diplotypes
M2	SSD	0.323	-	0.499	1100.73	ĀB ĀB
M3	SSD	0.332	0.947	0.500	1102.33	ĀB ĀB, ĀB BĀ
M1	SSD	0.323	1.000	0.500	1102.72	ĀB ĀB, ĀA ĀB, BĀ ĀB, ĀA BĀ, ĀB BA
M3	SSD	0.323	1.000	0.500	1102.73	ĀB ĀB, ĀA ĀB
M1	BSSD	0.041	0.752	0.500	1104.74	ĀB ĀB, ĀA ĀB, BĀ ĀB, ĀA BĀ, ĀB BA
M2	BSSD	0.044	-	0.500	1111.28	ĀB ĀB
M3	BSSD	0.043	0.852	0.500	1111.82	ĀB ĀB, ĀA ĀB
M3	BSSD	0.223	0.111	0.402	1170.46	ĀB ĀB, ĀB BĀ
M2	SSD	1.000	-	0.286	1225.77	ĀĀ ĀĀ
M2	BSSD	1.000	-	0.286	1225.77	ĀĀ ĀĀ
M1	BSSD	1.000	1.000	0.286	1227.77	ĀĀ ĀĀ, AĀ ĀĀ, BĀ ĀĀ, AĀ BĀ, AB ĀĀ
M3	BSSD	1.000	1.000	0.286	1227.77	ĀĀ ĀĀ, BĀ ĀĀ
M1	SSD	1.000	1.000	0.286	1227.77	ĀĀ ĀĀ, AĀ ĀĀ, BĀ ĀĀ, AĀ BĀ, AB ĀĀ
M3	BSSD	1.000	1.000	0.286	1227.77	ĀĀ ĀĀ, AĀ ĀĀ
M3	SSD	1.000	1.000	0.286	1227.77	ĀĀ ĀĀ, AĀ ĀĀ
M3	SSD	1.000	0.999	0.286	1227.85	ĀĀ ĀĀ, BĀ ĀĀ

Notation: Col = ĀA|ĀA , Cvi=BĀ|BĀ

Table S2. Results from the ML approach for the Sha \times Col cross. The tested models are ordered by decreasing AIC.

Sha \times Col

Model	Mode	w	w'	r	AIC	Incompatible diplotypes
M3	BSSD	0.124	0.738	0.500	1096.35	$\dot{A}\dot{B} \dot{A}\dot{B}$, $\dot{A}\dot{B} B\dot{B}$
M2	SSD	0.533	-	0.470	1097.12	$\dot{A}\dot{B} \dot{A}\dot{B}$
M1	BSSD	0.122	0.865	0.500	1098.47	$\dot{A}\dot{B} \dot{A}\dot{B}$, $\dot{A}A \dot{A}\dot{B}$, $B\dot{B} \dot{A}\dot{B}$, $\dot{A}A \dot{B}B$, $\dot{A}\dot{B} BA$
M2	BSSD	0.127	-	0.500	1098.70	$\dot{A}\dot{B} \dot{A}\dot{B}$
M3	SSD	0.534	0.994	0.470	1099.12	$\dot{A}\dot{B} \dot{A}\dot{B}$, $\dot{A}\dot{B} B\dot{B}$
M1	SSD	0.533	1.000	0.470	1099.12	$\dot{A}\dot{B} \dot{A}\dot{B}$, $\dot{A}A \dot{A}\dot{B}$, $B\dot{B} \dot{A}\dot{B}$, $\dot{A}A \dot{B}B$, $\dot{A}\dot{B} BA$
M3	SSD	0.533	1.000	0.470	1099.12	$\dot{A}\dot{B} \dot{A}\dot{B}$, $\dot{A}A \dot{A}\dot{B}$
M3	BSSD	0.126	0.932	0.500	1100.42	$\dot{A}\dot{B} \dot{A}\dot{B}$, $\dot{A}A \dot{A}\dot{B}$
M2	SSD	1.000	-	0.278	1168.52	$\dot{B}\dot{A} \dot{B}\dot{A}$
M2	BSSD	1.000	-	0.278	1168.52	$\dot{B}\dot{A} \dot{B}\dot{A}$
M1	BSSD	1.000	1.000	0.278	1170.52	$\dot{B}\dot{A} \dot{B}\dot{A}$, $A\dot{A} \dot{B}\dot{A}$, $\dot{B}B \dot{B}\dot{A}$, $A\dot{A} \dot{B}B$, $AB \dot{B}\dot{A}$
M3	BSSD	1.000	1.000	0.278	1170.52	$\dot{B}\dot{A} \dot{B}\dot{A}$, $A\dot{A} \dot{B}\dot{A}$
M3	BSSD	1.000	1.000	0.278	1170.52	$\dot{B}\dot{A} \dot{B}\dot{A}$, $\dot{B}B \dot{B}\dot{A}$
M3	SSD	1.000	1.000	0.278	1170.52	$\dot{B}\dot{A} \dot{B}\dot{A}$, $A\dot{A} \dot{B}\dot{A}$
M1	SSD	1.000	1.000	0.278	1170.53	$\dot{B}\dot{A} \dot{B}\dot{A}$, $A\dot{A} \dot{B}\dot{A}$, $\dot{B}B \dot{B}\dot{A}$, $A\dot{A} \dot{B}B$, $AB \dot{B}\dot{A}$
M3	SSD	1.000	0.999	0.278	1170.56	$\dot{B}\dot{A} \dot{B}\dot{A}$, $\dot{B}B \dot{B}\dot{A}$

Notation: Col = $\dot{A}A|\dot{A}A$, Sha= $B\dot{B}|\dot{B}B$

Table S3. Simulation results. (A) We simulated 100 experiments from model M2 (M2 SSD) using sample size (N), recombination fraction (r.true) and fitness (w.true). The estimated parameters (ML estimation) and their corresponding standard errors are shown. We also report the % of the time we were able to recover the correct incompatibility mode after having applied all alternative models; note that for w'=1 models M1 and M3 are equivalent to model M2; (B) We simulated 100 experiments from model M3 with biased single seed descent (M3 BSSD) using sample size (N), recombination fraction (r.true), fitness values w.true and w'.true. The estimated parameters and their corresponding standard errors are shown. We also report the % of the time we were able to recover the correct incompatibility mode after having applied all alternative models.

A

Model	N	r.true	w.true	w'.true	% correct model	w.bar	w.SEE	w'.bar	w'.SEE	r.bar	r.SEE
M2 SSD	350	0.4999	0.3	-	73	0.269	0.102	0.942	0.120	0.480	0.027
M2 SSD	350	0.3	0.3	-	67	0.228	0.133	0.915	0.135	0.300	0.036
M2 SSD	350	0.1	0.3	-	57	0.235	0.156	0.837	0.284	0.101	0.017
M2 SSD	1000	0.4999	0.3	-	64	0.272	0.096	0.941	0.096	0.485	0.022
M2 SSD	1000	0.3	0.3	-	68	0.251	0.105	0.941	0.101	0.301	0.023
M2 SSD	1000	0.1	0.3	-	62	0.270	0.124	0.919	0.124	0.099	0.011

B

Model	N	r.true	w.true	w'.true	% correct model	w.bar	w.SEE	w'.bar	w'.SEE	r.bar	r.SEE
M3 BSSD	350	0.4999	0.1	0.7	71	0.168	0.153	0.730	0.189	0.475	0.035
M3 BSSD	350	0.3	0.1	0.7	69	0.152	0.122	0.745	0.185	0.299	0.040
M3 BSSD	350	0.1	0.1	0.7	25	0.186	0.158	0.854	0.236	0.100	0.016
M3 BSSD	1000	0.4999	0.1	0.7	99	0.100	0.019	0.696	0.065	0.486	0.019
M3 BSSD	1000	0.3	0.1	0.7	93	0.110	0.053	0.718	0.091	0.298	0.026
M3 BSSD	1000	0.1	0.1	0.7	71	0.147	0.107	0.757	0.164	0.101	0.009